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Supplemental Information

Innate Immune Training of Granulopoiesis Promotes Anti-tumor Activity

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SUPPLEMENTARY TABLES

Table S1 (Related to Figure 2B). GSEA results.
Results of GSEA on RNA sequencing from tumor-associated neutrophils (TAN) derived from mice that were trained for 7 days with β-glucan or injected with PBS as control and were then inoculated with B16-F10 melanoma cells for 14 days, using a gene set of 92 genes, implicated as playing a role in the functionality of TAN-1 (derived from Shaul et al., 2016, specifically Table S4 therein; as described in the STAR methods). 86 genes out of the 92 gene set are expressed in our study and their position within our ranked list is shown. In addition, RANK METRIC SCORE refers to score used to position the gene in the ranked list, RUNNING ES refers to the enrichment score at this point in the ranked list of genes, and CORE ENRICHMENT describes whether the gene contributed to the leading-edge subset within the gene-set (i.e. the subset of genes that contributes most to the enrichment result).

Table S2 (Related to Figure 2D). GSEA results.
Results of GSEA on RNA sequencing from TAN derived from mice that were trained for 7 days with β-glucan or injected with PBS as control and were then inoculated with B16-F10 melanoma cells for 14 days, using the MSigDB Hallmark Gene Set. NAME is the gene set name; SIZE is the number of genes in the gene set after filtering out those genes not in the expression dataset; ES is the enrichment score for the gene set; NES is the normalized enrichment score that accounts for size differences in gene sets; NOM p-val is the nominal p-value of ES significance based on permutation test; FDR q-val is the False Discovery Rate; FWER p-val is the family-wise error rate; RANK AT MAX is the position in the ranked list at which the maximum running enrichment score occurred.

Table S3 (Related to Figure 4). The neutrophil bias of GMP upon β-glucan-induced trained immunity.
WT mice were treated with β-glucan or PBS and after 7 days BM GMP ($Lin^{-}c\text{-}Kit^{+}Sca1^{-}CD16/32^{+}CD34^{+}$) were sorted and RNA sequencing analysis was performed. The neutrophil bias of GMP was analyzed based on GSEA using the MSigDB Immunologic Signatures Gene Set. Datasets that include genes that are upregulated in neutrophils compared to other cell populations are shown in green and datasets with genes downregulated in neutrophils compared to other myeloid cell populations are shown in blue. Level of statistical significance was set at FDR = 0.05.
NAME is the gene set name; SIZE is the number of genes in the gene set after filtering out those genes not in the expression dataset; ES is the enrichment score for the gene set; NES is the normalized enrichment score that accounts for size differences in gene sets; NOM p-val is the nominal p-value of ES significance based on permutation test; FDR q-val is the False Discovery Rate; logFDR is the log value of FDR; FWER p-val is the family-wise error rate; RANK AT MAX is the position in the ranked list at which the maximum running enrichment score occurred.

Table S4 (Related to Figure 4G, H). GSEA results
Results of GSEA on RNA sequencing from GMP derived from mice that were trained for 7 days with β-glucan or injected with PBS as control using the MSigDB Hallmark

Gene Set. NAME is the gene set name; SIZE is the number of genes in the gene set after filtering out those genes not in the expression dataset; ES is the enrichment score for the gene set; NES is the normalized enrichment score that accounts for size differences in gene sets; NOM p-val is the nominal p-value of ES significance based on permutation test; FDR q-val is the False Discovery Rate; FWER p-val is the family-wise error rate; RANK AT MAX is the position in the ranked list at which the maximum running enrichment score occurred.

Table S5 (Related to STAR Methods). Gene-specific primers for the 'trained TAN1-like signature'

Gene-specific primers for the 'trained TAN1-like signature' used for quantitative real-time PCR analysis. The 'trained TAN1-like signature' is defined in 'STAR Methods' under 'RNA isolation and real time PCR'.

Table S1

	PROBE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
1	ENSMUSG00000020440	15	6.721	0.0686	Yes
2	ENSMUSG00000064373	44	5.321	0.1216	Yes
3	ENSMUSG00000021361	90	4.092	0.1604	Yes
4	ENSMUSG00000063856	105	3.820	0.1990	Yes
5	ENSMUSG00000036887	136	3.528	0.2332	Yes
6	ENSMUSG00000040212	163	3.222	0.2646	Yes
7	ENSMUSG00000023078	177	3.104	0.2957	Yes
8	ENSMUSG00000040950	179	3.078	0.3276	Yes
9	ENSMUSG00000024679	180	3.069	0.3595	Yes
10	ENSMUSG00000024570	243	2.703	0.3825	Yes
11	ENSMUSG00000024965	268	2.607	0.4077	Yes
12	ENSMUSG00000073421	322	2.446	0.4288	Yes
13	ENSMUSG00000036896	358	2.363	0.4505	Yes
14	ENSMUSG00000002741	443	2.079	0.4653	Yes
15	ENSMUSG00000030744	516	1.883	0.4790	Yes
16	ENSMUSG00000069516	519	1.878	0.4984	Yes
17	ENSMUSG00000032436	585	1.778	0.5116	Yes
18	ENSMUSG00000026728	681	1.605	0.5206	Yes
19	ENSMUSG00000031708	706	1.569	0.5349	Yes
20	ENSMUSG00000044533	809	1.442	0.5417	Yes
21	ENSMUSG00000002957	928	1.346	0.5461	Yes
22	ENSMUSG00000021190	998	1.291	0.5539	Yes
23	ENSMUSG00000002981	1004	1.284	0.5669	Yes
24	ENSMUSG00000027466	1029	1.249	0.5779	Yes
25	ENSMUSG00000057191	1082	1.201	0.5862	Yes
26	ENSMUSG00000061477	1100	1.182	0.5971	Yes
27	ENSMUSG00000028063	1221	1.078	0.5985	Yes
28	ENSMUSG00000030707	1253	1.053	0.6070	Yes
29	ENSMUSG00000030802	1322	1.008	0.6119	Yes
30	ENSMUSG00000032369	1350	0.987	0.6200	Yes
31	ENSMUSG00000060601	1477	0.921	0.6194	Yes
32	ENSMUSG00000021094	1520	0.883	0.6252	Yes
33	ENSMUSG00000056076	1590	0.851	0.6284	Yes
34	ENSMUSG00000035199	1656	0.818	0.6317	Yes
35	ENSMUSG00000021917	1666	0.814	0.6394	Yes
36	ENSMUSG00000020432	1671	0.809	0.6475	Yes
37	ENSMUSG00000063316	1676	0.808	0.6555	Yes
38	ENSMUSG00000036908	1678	0.806	0.6638	Yes
39	ENSMUSG00000037370	1709	0.790	0.6696	Yes
40	ENSMUSG00000018927	2005	0.680	0.6528	No
41	ENSMUSG00000026750	2219	0.594	0.6418	No
42	ENSMUSG00000003032	2386	0.536	0.6339	No
43	ENSMUSG00000033220	2519	0.492	0.6283	No
44	ENSMUSG00000026177	2726	0.439	0.6163	No
45	ENSMUSG00000031805	2735	0.438	0.6202	No
46	ENSMUSG00000001056	2862	0.409	0.6142	No
47	ENSMUSG00000029470	2930	0.390	0.6129	No
48	ENSMUSG00000034786	3142	0.337	0.5993	No
49	ENSMUSG00000007564	3340	0.293	0.5864	No
50	ENSMUSG00000016319	3363	0.287	0.5876	No
51	ENSMUSG00000051695	3574	0.249	0.5732	No
52	ENSMUSG00000035493	3588	0.247	0.5747	No
53	ENSMUSG00000089832	3641	0.239	0.5730	No
54	ENSMUSG00000060743	3721	0.227	0.5690	No
55	ENSMUSG00000067212	3795	0.214	0.5653	No

56	ENSMUSG00000075705	3930	0.193	0.5565	No
57	ENSMUSG00000023067	4147	0.163	0.5407	No
58	ENSMUSG00000029528	4349	0.140	0.5259	No
59	ENSMUSG00000025491	4386	0.136	0.5244	No
60	ENSMUSG00000017057	4628	0.112	0.5061	No
61	ENSMUSG00000022831	4707	0.103	0.5008	No
62	ENSMUSG00000015714	4933	0.078	0.4834	No
63	ENSMUSG00000004934	4989	0.072	0.4797	No
64	ENSMUSG00000022090	5048	0.065	0.4757	No
65	ENSMUSG00000037731	5197	0.046	0.4642	No
66	ENSMUSG00000026158	6669	0.000	0.3453	No
67	ENSMUSG00000032324	7306	-0.038	0.2943	No
68	ENSMUSG00000055413	7313	-0.039	0.2942	No
69	ENSMUSG00000025351	7499	-0.058	0.2799	No
70	ENSMUSG00000029723	7639	-0.074	0.2694	No
71	ENSMUSG00000029621	8670	-0.191	0.1881	No
72	ENSMUSG00000036620	9418	-0.316	0.1310	No
73	ENSMUSG00000027333	9443	-0.319	0.1324	No
74	ENSMUSG00000028494	9488	-0.327	0.1322	No
75	ENSMUSG00000029064	9644	-0.362	0.1234	No
76	ENSMUSG00000052423	9667	-0.368	0.1255	No
77	ENSMUSG00000021453	9761	-0.394	0.1220	No
78	ENSMUSG00000021134	9965	-0.446	0.1103	No
79	ENSMUSG00000038467	9998	-0.454	0.1124	No
80	ENSMUSG00000021998	10131	-0.490	0.1068	No
81	ENSMUSG00000034855	10876	-0.797	0.0549	No
82	ENSMUSG00000054808	10919	-0.823	0.0601	No
83	ENSMUSG00000028249	10997	-0.867	0.0629	No
84	ENSMUSG00000020946	11396	-1.222	0.0434	No
85	ENSMUSG00000031207	11546	-1.427	0.0461	No
86	ENSMUSG00000021196	11986	-2.618	0.0378	No

Table S2

	NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
1	HALLMARK_XENOBIOTIC_METABOLISM	153	0.57	1,89	0.000	0.000	0.000	2585	tags=36%, list=21%, signal=45%
2	HALLMARK_COAGULATION	103	0.57	1,74	0.000	0.006	0.006	1973	tags=34%, list=16%, signal=40%
3	HALLMARK_COMPLEMENT	150	0.51	1,66	0.000	0.015	0.021	1973	tags=28%, list=16%, signal=33%
4	HALLMARK_ALLOGRAFT_REJECTION	160	0.49	1,63	0.000	0.016	0.029	2067	tags=28%, list=17%, signal=33%
5	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	143	0.46	1,50	0.004	0.055	0.129	2024	tags=29%, list=16%, signal=34%
6	HALLMARK_ANGIOGENESIS	30	0.59	1,49	0.033	0.048	0.133	2070	tags=40%, list=17%, signal=48%
7	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY	42	0.54	1,45	0.044	0.061	0.202	2638	tags=40%, list=21%, signal=51%
8	HALLMARK_BILE_ACID_METABOLISM	83	0.48	1,44	0.018	0.056	0.212	2170	tags=35%, list=17%, signal=42%
9	HALLMARK_OXIDATIVE_PHOSPHORYLATION	188	0.41	1,41	0.005	0.069	0.269	2565	tags=38%, list=21%, signal=47%
10	HALLMARK_FATTY_ACID_METABOLISM	126	0.43	1,38	0.022	0.081	0.334	1120	tags=17%, list=9%, signal=18%
11	HALLMARK_UV_RESPONSE_UP	115	0.37	1,19	0.109	0.339	0.865	709	tags=12%, list=6%, signal=13%
12	HALLMARK_PEROXISOME	79	0.40	1,17	0.164	0.345	0.891	2240	tags=33%, list=18%, signal=40%
13	HALLMARK_KRAS_SIGNALING_UP	140	0.34	1,11	0.212	0.483	0.970	2535	tags=28%, list=20%, signal=35%
14	HALLMARK_INFLAMMATORY_RESPONSE	163	0.33	1,10	0.202	0.471	0.977	2200	tags=21%, list=18%, signal=26%
15	HALLMARK_INTERFERON_GAMMA_RESPONSE	174	0.32	1,10	0.190	0.450	0.978	1924	tags=24%, list=15%, signal=27%
16	HALLMARK_APOPTOSIS	144	0.33	1,08	0.227	0.476	0.986	1654	tags=18%, list=13%, signal=21%
17	HALLMARK_ADIPOGENESIS	183	0.30	1.00	0.443	0.688	0.998	2613	tags=32%, list=21%, signal=40%
18	HALLMARK_PI3K_AKT_MTOR_SIGNALING	92	0.33	0.98	0.485	0.726	0.999	1175	tags=15%, list=9%, signal=17%
19	HALLMARK_MTORC1_SIGNALING	190	0.29	0.96	0.593	0.771	1.000	1253	tags=12%, list=10%, signal=13%
20	HALLMARK_IL2_STAT5_SIGNALING	170	0.29	0.95	0.598	0.771	1.000	1134	tags=12%, list=9%, signal=13%
21	HALLMARK_MYOGENESIS	128	0.28	0.92	0.717	0.848	1.000	1441	tags=12%, list=12%, signal=13%
22	HALLMARK_MYC_TARGETS_V1	195	0.27	0.91	0.743	0.827	1.000	1632	tags=17%, list=13%, signal=19%
23	HALLMARK_IL6_JAK_STAT3_SIGNALING	76	0.30	0.89	0.653	0.851	1.000	1977	tags=18%, list=16%, signal=22%
24	HALLMARK_P53_PATHWAY	175	0.26	0.88	0.848	0.845	1.000	2720	tags=23%, list=22%, signal=29%
25	HALLMARK_APICAL_JUNCTION	130	0.26	0.83	0.917	0.944	1.000	2335	tags=22%, list=19%, signal=27%
26	HALLMARK_HEDGEHOG_SIGNALING	24	0.34	0.80	0.764	0.943	1.000	832	tags=13%, list=7%, signal=13%
27	HALLMARK_NOTCH_SIGNALING	26	0.33	0.79	0.799	0.919	1.000	762	tags=8%, list=6%, signal=8%

Table S3

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	logFDR	FWER p-val	RANK AT MAX	LEADING EDGE
GSE3982_NEUTROPHIL_VS_BASOPHIL_UP	127	0.18792799	2.4936059	0.0	0,002506787	-2,6009	0.706	4141	tags=54%, list=36%, signal=84%
GSE27786_NEUTROPHIL_VS_MONO_MAC_UP	147	0.17262954	2.4513268	0.0	0,00330879	-2,4803	0.819	4488	tags=56%, list=39%, signal=90%
GSE22886_NEUTROPHIL_VS_MONOCYTE_DN	186	-0.21431348	-3.4768302	0.0	0,0000001	-7	0.0	3476	tags=51%, list=30%, signal=72%
GSE22886_NEUTROPHIL_VS_DC_DN	187	-0.19650963	-3.0743666	0.0	1,79E-05	-4,7464	0.008	4701	tags=60%, list=41%, signal=99%
GSE27786_NEUTROPHIL_VS_MONO_MAC_DN	163	-0.13489847	-2.0292807	0.0039525	0,02150858	-1,6674	1.0	6351	tags=68%, list=55%, signal=149%
GSE3982_NEUTROPHIL_VS_BASOPHIL_DN	164	-0.13247892	-1.9812163	0.0057361	0,027381597	-1,5625	1.0	6260	tags=67%, list=54%, signal=144%

Table S4

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
HALLMARK_ADIPOGENESIS	185	-0.33846906	-1.3614275	0.013333334	0.28227615	1.0	4268	tags=39%, list=21%, signal=49%
HALLMARK_COAGULATION	100	-0.33541805	-1.2790787	0.052173913	0.34569374	1.0	1235	tags=17%, list=6%, signal=18%
HALLMARK_DNA_REPAIR	137	-0.34788033	-1.3801625	0.014851485	0.26497552	1.0	5882	tags=47%, list=29%, signal=66%
HALLMARK_E2F_TARGETS	194	-0.31480807	-1.3173583	0.0062111802	0.3153329	1.0	3084	tags=28%, list=15%, signal=33%
HALLMARK_FATTY_ACID_METABOLISM	135	-0.4787959	-1.9237534	0.0	0.004593605	0.644	3068	tags=32%, list=15%, signal=37%
HALLMARK_GLYCOLYSIS	179	-0.26821175	-1.0679168	0.270073	0.552309	1.0	3069	tags=23%, list=15%, signal=27%
HALLMARK_HEME_METABOLISM	182	-0.4612496	-1.8512348	0.0	0.011261245	0.962	3668	tags=43%, list=18%, signal=52%
HALLMARK_MYC_TARGETS_V1	191	-0.5460221	-2.215301	0.0	2.1171085E-5	0.002	4388	tags=50%, list=21%, signal=63%
HALLMARK_MYC_TARGETS_V2	56	-0.2756289	-0.93721586	0.5738832	0.7502626	1.0	5078	tags=32%, list=25%, signal=43%
HALLMARK_OXIDATIVE_PHOSPHORYLATION	192	-0.6128583	-2.4825552	0.0	0.0	0.0	3337	tags=48%, list=16%, signal=57%
HALLMARK_PANCREAS_BETA_CELLS	16	-0.37138817	-0.9443386	0.5298507	0.738289	1.0	3887	tags=44%, list=19%, signal=54%
HALLMARK_PEROXISOME	87	-0.32129171	-1.1875292	0.104417674	0.43081608	1.0	3737	tags=25%, list=18%, signal=31%
HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY	45	-0.3314567	-1.0733126	0.3138686	0.5458442	1.0	1475	tags=22%, list=7%, signal=24%
HALLMARK_SPERMATOGENESIS	95	-0.3639183	-1.3378547	0.034042552	0.30096272	1.0	2540	tags=19%, list=12%, signal=22%
HALLMARK_XENOBIOTIC_METABOLISM	156	-0.34734932	-1.3840812	0.005319149	0.26299122	1.0	3148	tags=27%, list=15%, signal=32%
HALLMARK_ALLOGRAFT_REJECTION	170	0.46404052	1.5719068	0.0023501762	0.052239303	1.0	2577	tags=29%, list=13%, signal=33%
HALLMARK_ANDROGEN_RESPONSE	89	0.39515847	1.2371061	0.12663186	0.27786115	1.0	4638	tags=36%, list=23%, signal=46%
HALLMARK_ANGIOGENESIS	30	0.4034587	1.0658443	0.3589365	0.5110081	1.0	1217	tags=23%, list=6%, signal=25%
HALLMARK_APICAL_JUNCTION	154	0.3940256	1.3250257	0.032104637	0.19279501	1.0	3326	tags=24%, list=16%, signal=28%
HALLMARK_APICAL_SURFACE	34	0.39776358	1.0732794	0.35548687	0.50010306	1.0	3977	tags=38%, list=19%, signal=47%
HALLMARK_APOPTOSIS	142	0.37509593	1.2475381	0.0964591	0.26687083	1.0	3111	tags=27%, list=15%, signal=32%
HALLMARK_BILE_ACID_METABOLISM	90	0.28031233	0.895026	0.65653896	0.7631104	1.0	3121	tags=19%, list=15%, signal=22%
HALLMARK_CHOLESTEROL_HOMEOSTASIS	65	0.3066085	0.93213403	0.59172416	0.7101496	1.0	3408	tags=23%, list=17%, signal=28%
HALLMARK_COMPLEMENT	162	0.56313586	1.879213	0.0	0.0022028668	0.573	3401	tags=38%, list=17%, signal=45%
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	162	0.33245185	1.1169387	0.24357405	0.43610907	1.0	2355	tags=16%, list=11%, signal=18%
HALLMARK_ESTROGEN_RESPONSE_EARLY	165	0.3664692	1.245726	0.082825825	0.26891556	1.0	4005	tags=28%, list=19%, signal=35%
HALLMARK_ESTROGEN_RESPONSE_LATE	158	0.3027445	1.0176535	0.41428572	0.58285004	1.0	2845	tags=21%, list=14%, signal=24%
HALLMARK_G2M_CHECKPOINT	190	0.31091806	1.0591061	0.3479769	0.52160436	1.0	4276	tags=31%, list=21%, signal=39%
HALLMARK_HEDGEHOG_SIGNALING	28	0.570338	1.4751666	0.03598201	0.09293582	1.0	4459	tags=57%, list=22%, signal=73%
HALLMARK_HYPOXIA	172	0.4015272	1.3718623	0.020190023	0.1560477	1.0	3392	tags=27%, list=16%, signal=32%
HALLMARK_IL2_STAT5_SIGNALING	186	0.39008537	1.3308102	0.036599763	0.18805379	1.0	3324	tags=30%, list=16%, signal=36%
HALLMARK_IL6_JAK_STAT3_SIGNALING	76	0.62220806	1.9157144	0.0	0.0012145527	0.326	1563	tags=38%, list=8%, signal=41%
HALLMARK_INFLAMMATORY_RESPONSE	171	0.6786922	2.2992964	0.0	0.0	0.0	3358	tags=50%, list=16%, signal=60%
HALLMARK_INTERFERON_ALPHA_RESPONSE	87	0.7168267	2.2577653	0.0	0.0	0.0	2231	tags=44%, list=11%, signal=49%
HALLMARK_INTERFERON_GAMMA_RESPONSE	179	0.6370029	2.1780353	0.0	0.0	0.0	2577	tags=41%, list=13%, signal=46%

HALLMARK_KRAS_SIGNALING_DN	99	0.36303	1.153687	0.21501273	0.3836147	1.0	3617	tags=26%, list=18%, signal=32%
HALLMARK_KRAS_SIGNALING_UP	156	0.3227955	1.0742397	0.32555282	0.49895805	1.0	3324	tags=26%, list=16%, signal=30%
HALLMARK_MITOTIC_SPINDLE	197	0.5210862	1.8103101	0.0	0.0057318024	0.976	4044	tags=38%, list=20%, signal=47%
HALLMARK_MTORC1_SIGNALING	194	0.29150614	1.0057975	0.4749709	0.60129726	1.0	3822	tags=26%, list=19%, signal=32%
HALLMARK_MYOGENESIS	148	0.23314323	0.780032	0.8951132	0.90023285	1.0	3399	tags=20%, list=16%, signal=23%
HALLMARK_NOTCH_SIGNALING	30	0.41829374	1.1076216	0.33333334	0.4495052	1.0	2864	tags=27%, list=14%, signal=31%
HALLMARK_P53_PATHWAY	185	0.39183876	1.3434826	0.025974026	0.17812084	1.0	2544	tags=23%, list=12%, signal=26%
HALLMARK_PI3K_AKT_MTOR_SIGNALING	95	0.51282907	1.6282574	0.0025839794	0.035768677	1.0	2160	tags=23%, list=10%, signal=26%
HALLMARK_PROTEIN_SECRETION	92	0.44095328	1.3757209	0.051587302	0.15286866	1.0	3282	tags=26%, list=16%, signal=31%
HALLMARK_TGF_BETA_SIGNALING	50	0.37458792	1.0818352	0.33994335	0.48809466	1.0	3144	tags=28%, list=15%, signal=33%
HALLMARK_TNFA_SIGNALING_VIA_NFKB	183	0.5215684	1.7845715	0.0	0.008045328	0.998	3144	tags=36%, list=15%, signal=42%
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	105	0.37609214	1.2050011	0.14133333	0.3157383	1.0	3372	tags=24%, list=16%, signal=28%
HALLMARK_UV_RESPONSE_DN	131	0.4610755	1.5076544	0.0024271845	0.07844182	1.0	2046	tags=22%, list=10%, signal=24%
HALLMARK_UV_RESPONSE_UP	132	0.32200328	1.0633616	0.33736396	0.51492196	1.0	4348	tags=30%, list=21%, signal=37%
HALLMARK_WNT_BETA_CATENIN_SIGNALING	37	0.42813328	1.170017	0.2392638	0.3607959	1.0	2198	tags=22%, list=11%, signal=24%

Table S5

Oligonucleotides

FW *Arf5*	5'-ATGCGGCTGGCAAGACTAC-3'
RV *Arf5*	5'-ACAGAGGCCGAATCTTATCCT-3'
FW *Selenop*	5'-AGCTCTGCTTGTTACAAAGCC-3'
RV *Selenop*	5'-CAGGTCTTCCAATCTGGATGC-3'
FW *C1qa*	5'-AAAGGCAATCCAGGCAATATCA-3'
RV *C1qa*	5'-TGGTTCTGGTATGGACTCTCC-3'
FW *Cxcl13*	5'-GGCCACGGTATTCTGGAAGC-3'
RV *Cxcl13*	5'-GGGCGTAACTTGAATCCGATCTA-3'
FW *Mgl2*	5'-TTAGCCAATGTGCTTAGCTGG-3'
RV *Mgl2*	5'-GGCCTCCAATTCTTGAAACCT-3'
FW *Ms4a6d*	5'-TTCCATCCTGTTAGAATCTGGCT-3'
RV *Ms4a6d*	5'-GTGAACCAAAGGCTTAGTCATCT-3'
FW *Rbfa*	5'-GCCATCCAAGCATGAGTTCCT-3'
RV *Rbfa*	5'-AGCAGTTCCGTCAATGATTTGTA-3'
FW *H2-Ab1*	5'-TGAACAGCCCAATGTCGTCAT-3'
RV *H2-Ab1*	5'-CAGCGCACTTTGATCTTGGC-3'
FW *C1qc*	5'-AGAAGCACCAGTCGGTATTCA-3'
RV *C1qc*	5'-TGCGATGTGTAGTAGACGAAGTA-3'
FW *Ykt6*	5'-AGTCAACTGATTGTGGAACGC-3'
RV *Ykt6*	5'-TCTGGAAGGGTATTCGCTGTC-3'
FW *Tmem14c*	5'-CAGTGGCCCATTGATGCCTT-3'
RV *Tmem14c*	5'-GACGGCACACTACCTGCTT-3'
FW *Gpx1*	5'-AGTCCACCGTGTATGCCTTCT-3'
RV *Gpx1*	5'-GAGACGCGACATTCTCAATGA-3'
FW *Emp3*	5'-TGGTGCTGTCTCTCATCCTCT-3'
RV *Emp3*	5'-CGAAGCAGTAACCGAAGCTG-3'
FW *Fermt3*	5'-ATGGCGGGTATGAAGACAGC-3'
RV *Fermt3*	5'-CACCAATGTGCGACTCCCC-3'
FW *Lyz2*	5'-ATGGAATGGCTGGCTACTATGG-3'
RV *Lyz2*	5'-ACCAGTATCGGCTATTGATCTGA-3'
FW *Cmtm7*	5'-TCCAAGAGTTACAACCAGAGTGG-3'
RV *Cmtm7*	5'-CACAAGCTCGCTAGGCAGAG-3'
FW *Vim*	5'-CGGCTGCGAGAGAAATTGC-3'
RV *Vim*	5'-CCACTTTCCGTTCAAGGTCAAG-3'
FW *Tecr*	5'-AAGCACTACGAGGTGGAGATT-3'
RV *Tecr*	5'-TGAGGCTCTACCTTGTCCAGG-3'
FW *Ap2a2*	5'-ACAGATACACGGAAAAGCAGATT-3'
RV *Ap2a2*	5'-ACCCATAAACGTAGGATTGCG-3'
FW *Rps3*	5'-ATGGCGGTGCAGATTTCCAA-3'
RV *Rps3*	5'-GTAACTCGGACTTCAACTCCAG-3'